FIG. 1

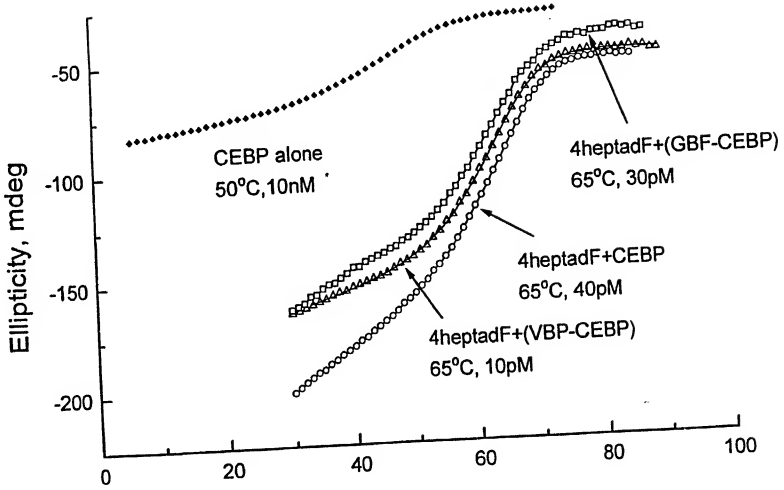


FIG. 2

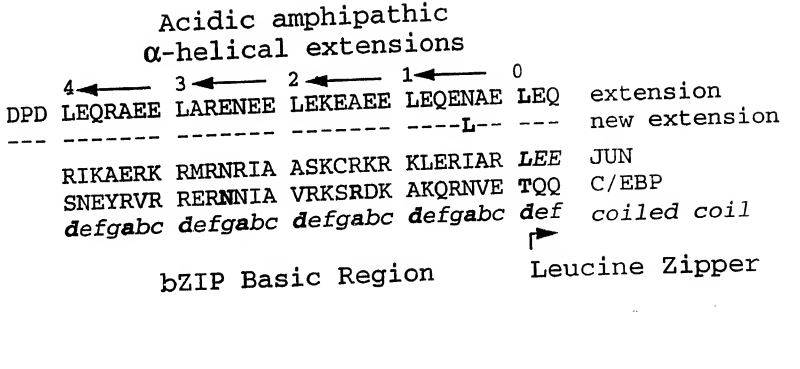


FIG. 3

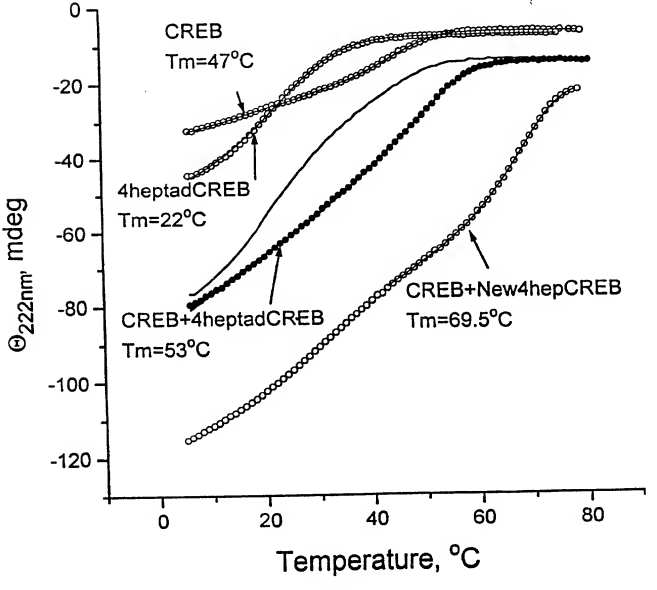

CREB
Tm=47°C
4heptadCREB
Tm=22°C
CREB+4heptadCREB
Tm=53°C
CREB+New4hepCREB
Tm=69.5°C
Θ222nm, mdeg
Temperature, °C
0
-20
-40
-60
-80
-100
-120
0
20
40
60
80

FIG. 4

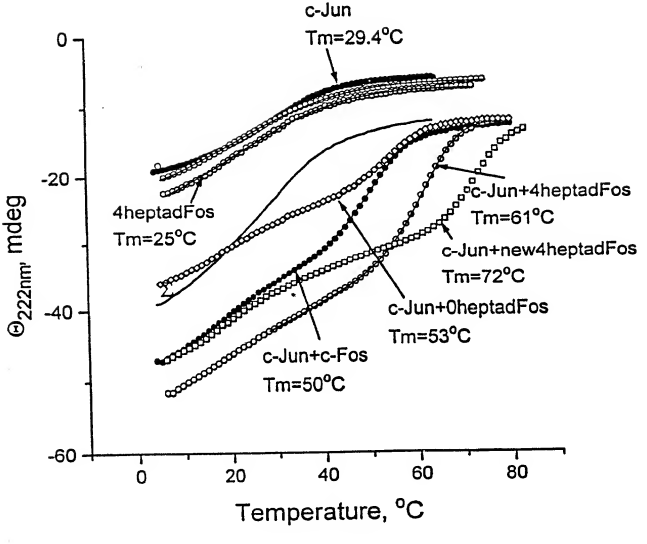


FIG. 5A

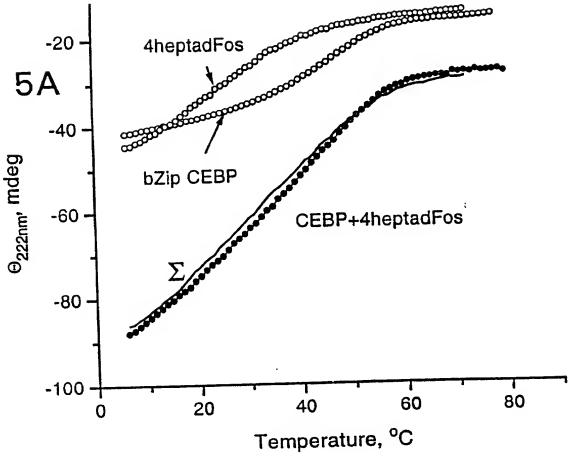


FIG. 5B

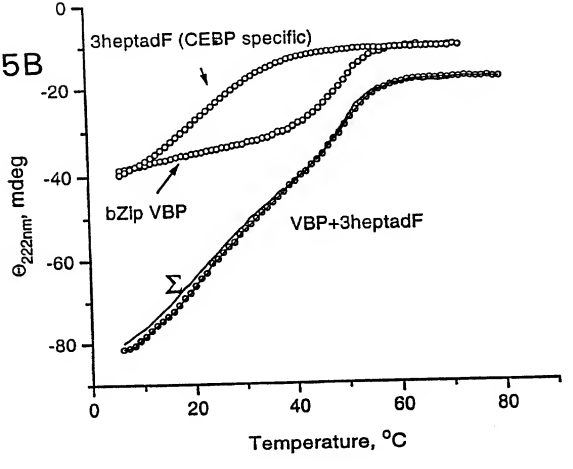


FIG. 6

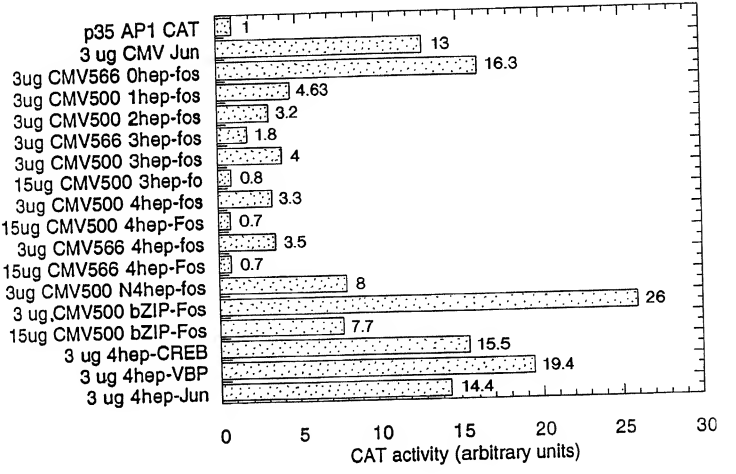
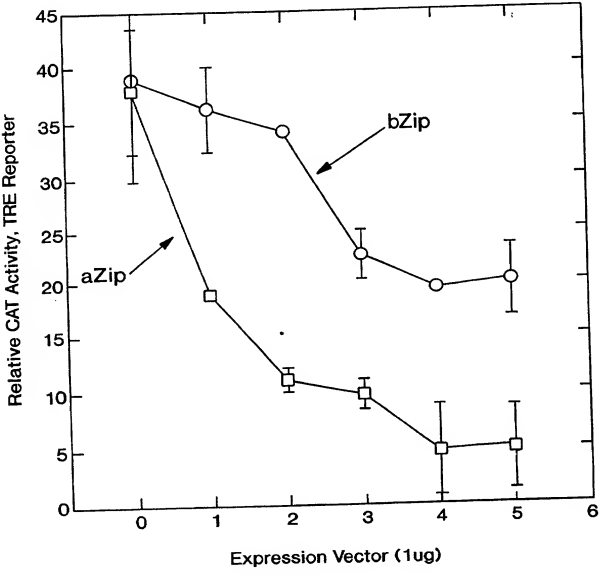


FIG. 7


Relative CAT Activity, TRE Reporter
45
40
35
30
25
20
15
10
5
0
bZip
aZip
0
1
2
3
4
5
6
Expression Vector (1ug)

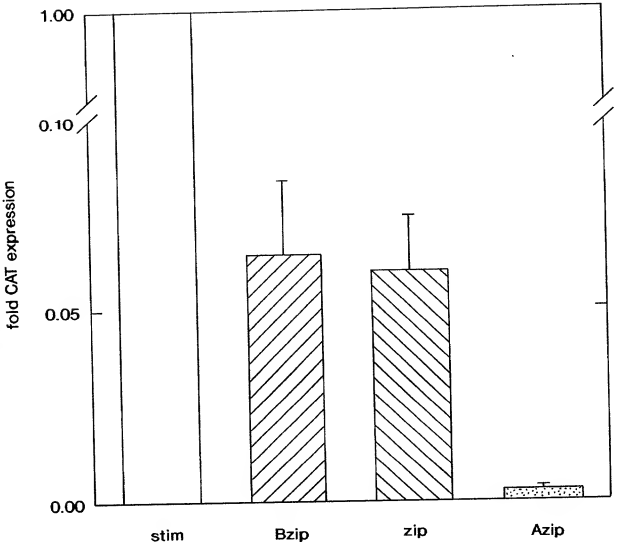


FIG. 8

FIG. 9

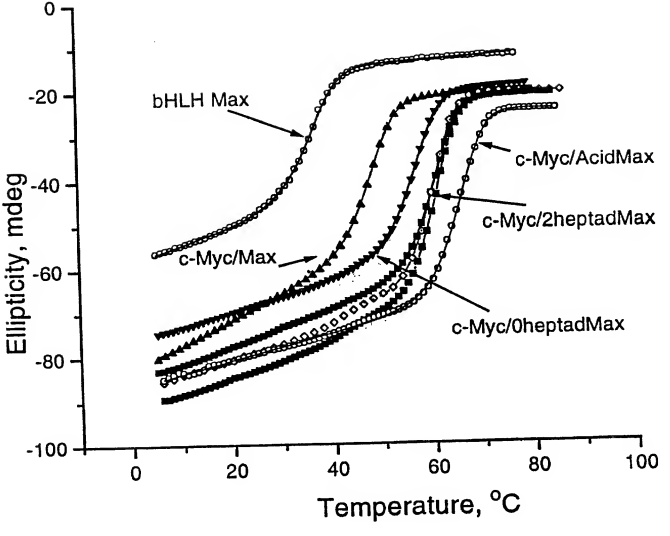


FIG. 10A

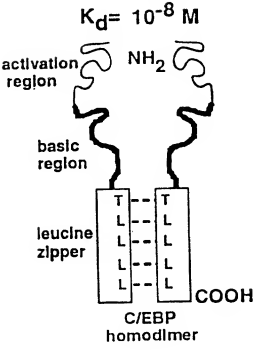
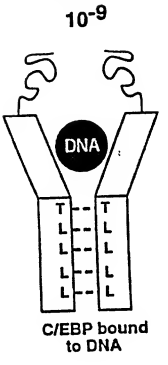


FIG. 10B



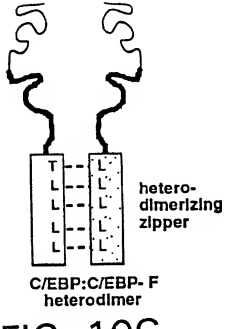


FIG. 10C

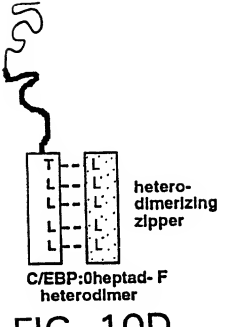


FIG. 10D

FIG. 11A

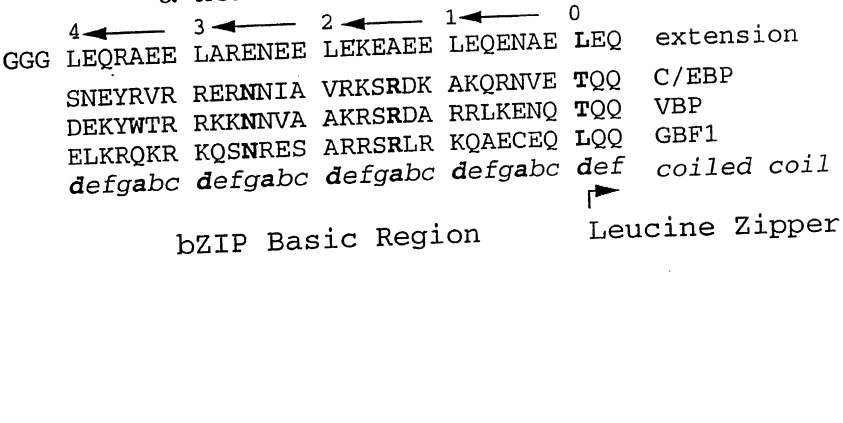


FIG. 11B

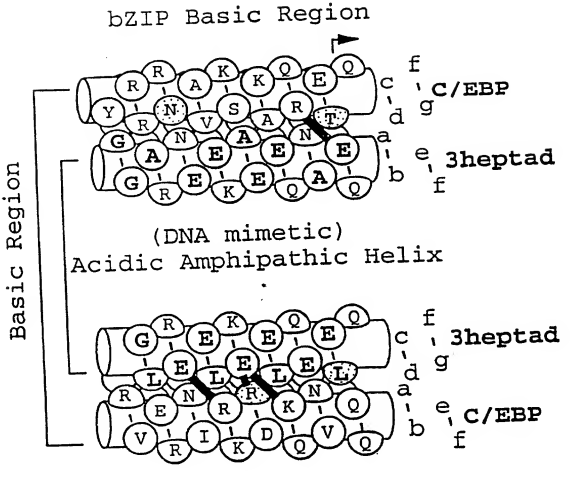


FIG. 11C

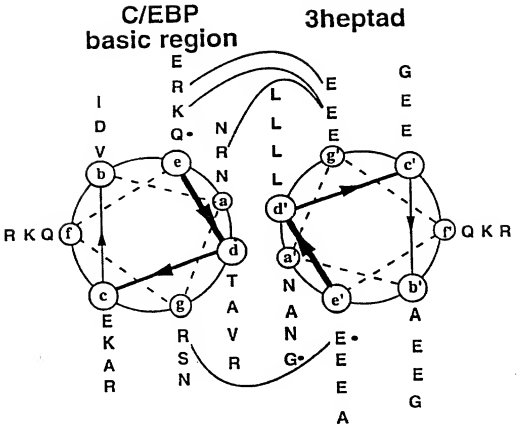

C/EBP
basic region
3heptad
E
R
K
Q
N
R
N
I
D
V
b
e
a
R K Q
f
d
T
A
V
R
c
g
E
K
A
R
R
S
N
L
L
L
L
d'
a'
N
A
N
G
E
E
E
A
E
E
G
g'
c'
r'
Q K R
e'
b'
A
E
E
G

FIG. 12

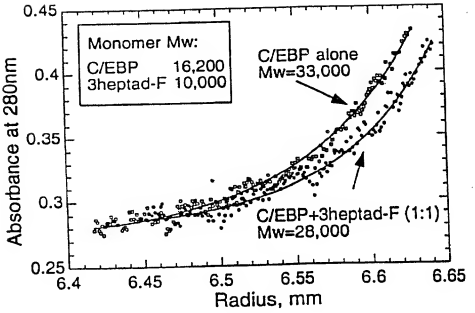
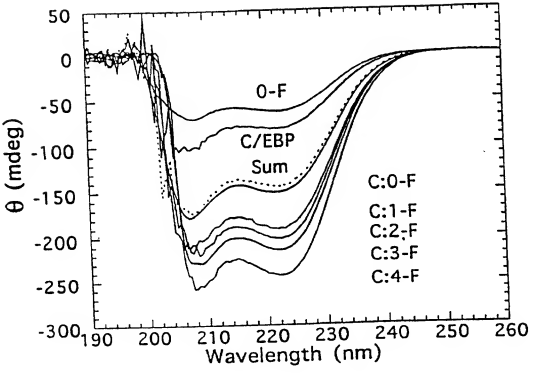

Monomer Mw:
C/EBP 16,200
3heptad-F 10,000
C/EBP alone
Mw=33,000
C/EBP+3heptad-F (1:1)
Mw=28,000
Absorbance at 280nm
Radius, mm
0.45
0.4
0.35
0.3
0.25
6.4
6.45
6.5
6.55
6.6
6.65

FIG. 13A



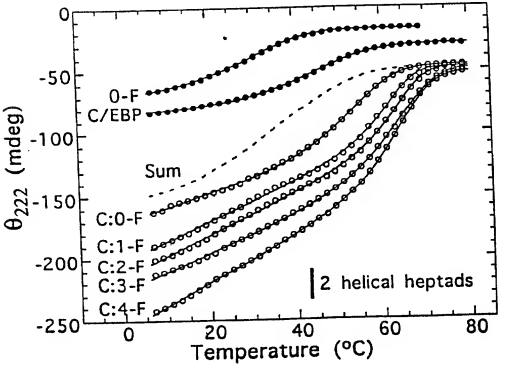


FIG. 13B

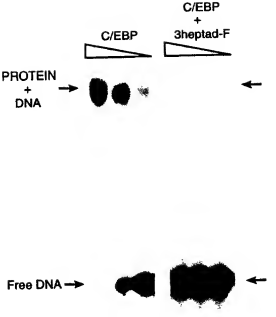


FIG. 14A

FIG. 14B

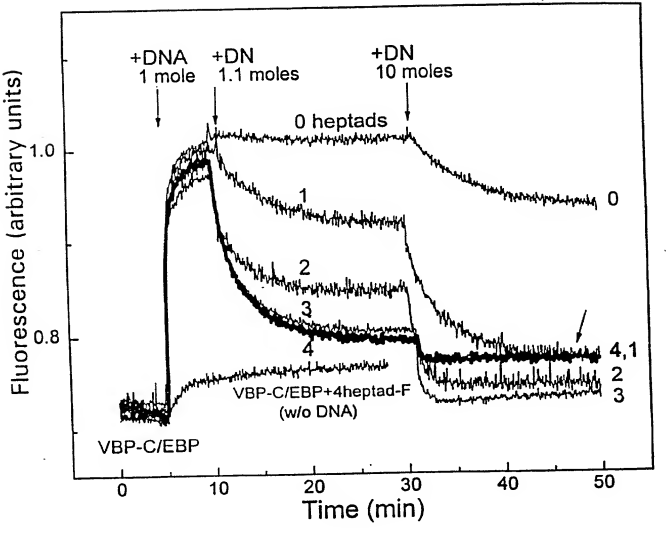

+DNA
1 mole
+DN
1.1 moles
+DN
10 moles
0 heptads
1
2
3
4
0
4,1
2
3
VBP-C/EBP+4heptad-F
(w/o DNA)
VBP-C/EBP
Fluorescence (arbitrary units)
1.0
0.8
0
10
20
30
40
50
Time (min)

FIG. 15

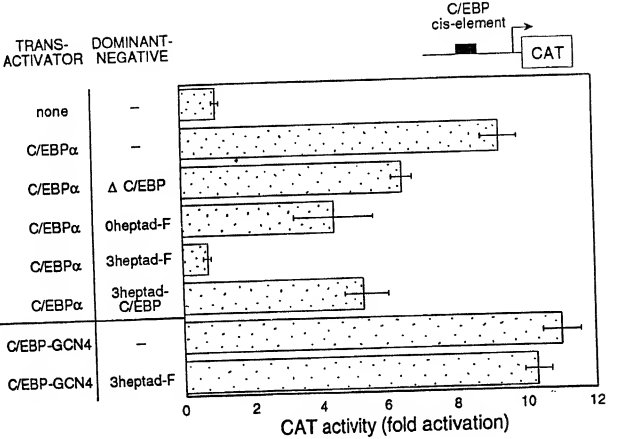

C/EBP
cis-element
CAT
TRANS-ACTIVATOR
DOMINANT-NEGATIVE
none
–
C/EBPα
–
C/EBPα
Δ C/EBP
C/EBPα
0heptad-F
C/EBPα
3heptad-F
C/EBPα
3heptad-C/EBP
C/EBP-GCN4
–
C/EBP-GCN4
3heptad-F
0
2
4
6
8
10
12
CAT activity (fold activation)

FIG. 16A

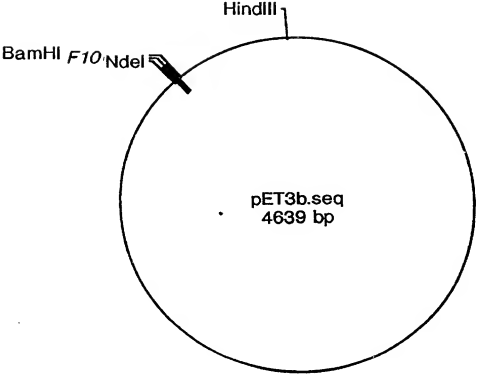
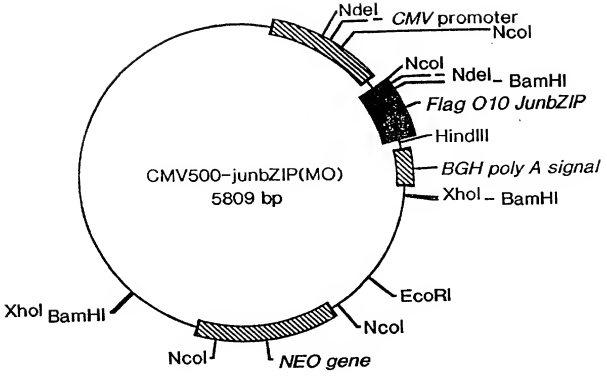


FIG. 16B



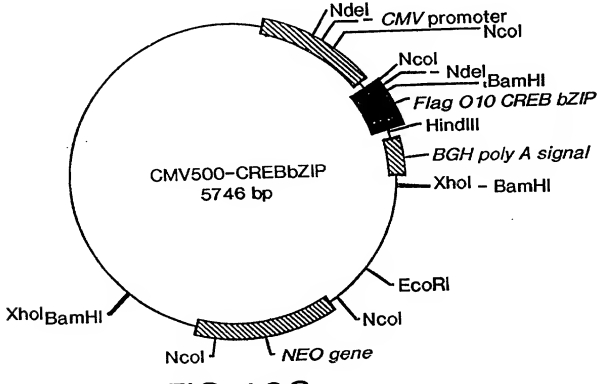


FIG. 16C

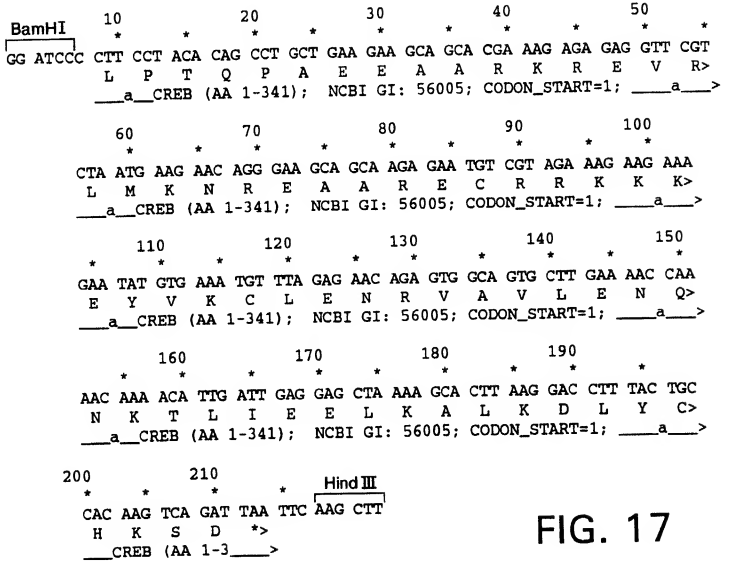


FIG. 17

```
900          910          920          930          940
   * NcoI *
CC ATG GAC TAC AAG GAC GAC GAT GAC AAG CAT ATG GCT AGC ATG ACT GGT
   M   D   Y   K   D   D   D   D   K   H   M   A   S   M   T   G>
   M   D   Y   K   D   D   D   D   K   H   M   A   S   M   T   G>

950          960          970          980          990
GGA CAG CAA ATG GGT CGG GAT CCC CTT CCT ACA CAG CCT GCT GAA GAA
 G   Q   Q   M   G   R   D   P   L   P   T   Q   P   A   E   E>
 G   Q   Q   M   G   R   D   P   L   P   T   Q   P   A   E   E>

1000         1010         1020         1030         1040
GCA GCA CGA AAG AGA GAG GTT CGT CTA ATG AAG AAC AGG GAA GCA GCA
 A   A   R   K   R   E   V   R   L   M   K   N   R   E   A   A>
 A   A   R   K   R   E   V   R   L   M   K   N   R   E   A   A>

1050         1060         1070         1080         1090
AGA GAA TGT CGT AGA AAG AAG AAA GAA TAT GTG AAA TGT TTA GAG AAC
 R   E   C   R   R   K   K   K   E   Y   V   K   C   L   E   N>
 R   E   C   R   R   K   K   K   E   Y   V   K   C   L   E   N>

1100         1110         1120         1130
AGA GTG GCA GTG CTT GAA AAC CAA AAC AAA ACA TTG ATT GAG GAG CTA
 R   V   A   V   L   E   N   Q   N   K   T   L   I   E   E   L>
 R   V   A   V   L   E   N   Q   N   K   T   L   I   E   E   L>

1140         1150         1160         1170         1180
AAA GCA CTT AAG GAC CTT TAC TGC CAC AAG TCA GAT TAA TTC AAG CTT
 K   A   L   K   D   L   Y   C   H   K   S   D   *          * Hind III
 K   A   L   K   D   L   Y   C   H   K   S   D   *
```

FIG. 18

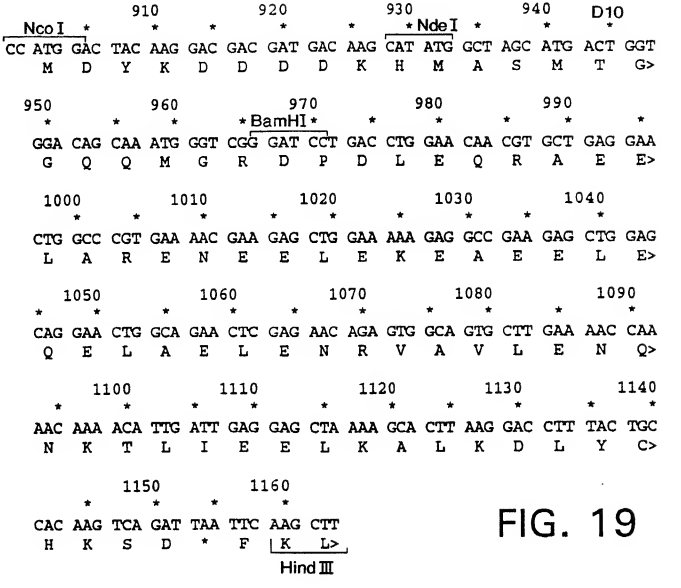


FIG. 19

```
BamH I    10                20              30              40
      *      *        *        *       *        *        *       *        *
GGATCCC AAG GTG GAA CAG TTA TCT CCA GAA GAA GAA GAG AAA AGG AGA
  P   D   K   V   E   Q>
                          L   S   P   E   E   E   E   K   R   R>
      ___1783 TO ____>
                        __2470_2466 TO 2573 OF HUM FOS _0__b___>

50              60              70                80              90
 *       *        *        *       *       *        *       *        *       *
ATC CGA AGG GAA AGG AAT AAG ATG GCT GCA GCC AAA TGC CGC AAC CGG
 I   R   R   E   R   N   K   M   A   A   A   K   C   R   N   R>
__2500_b___b___251_2466 TO 2573 OF HUM FOS _30_b___b___2540b___>

100              110             120             130              140
 *       *        *       *       *        *       *        *       *       *
AGG AGG GAG CTG ACT GAT ACA CTC CAA GCG GAG ACA GAC CAA CTA GAA
 R   R   E   L   T   D   T   L   Q   A>
                                         E   T   D   Q   L   E>
___b_2_2466 TO 2573 OF HUM FOS _570b___>
                                    26_2688 TO 3329 OF H____>

    150             160              170             180              190
     *        *       *        *       *        *       *        *       *
GAT GAG AAG TCT GCT TTG CAG ACC GAG ATT GCC AAC CTG CTG AAG GAG
 D   E   K   S   A   L   Q   T   E   I   A   N   L   L   K   E>
__2710_c___c___272_2688 TO 3329 OF HUM FOS _40_c___c___2750c___>

       200             210              220              230              240
 *        *       *        *       *        *       *        *       *        *
AAG GAA AAA CTA GAG TTC ATC CTG GCA GCT CAC CGA CCT GCC TGC AAG
 K   E   K   L   E   F   I   L   A   A   H   R   P   A   C   K>
___c_2760__c___c___2688 TO 3329 OF HUM FOS __2790__c___c__2800_>

        250         260
     *       *       *       *
ATC CCT GAT TAATTCAAGC TT
 I   P>                 Hind III
___c___>
```

FIG. 20

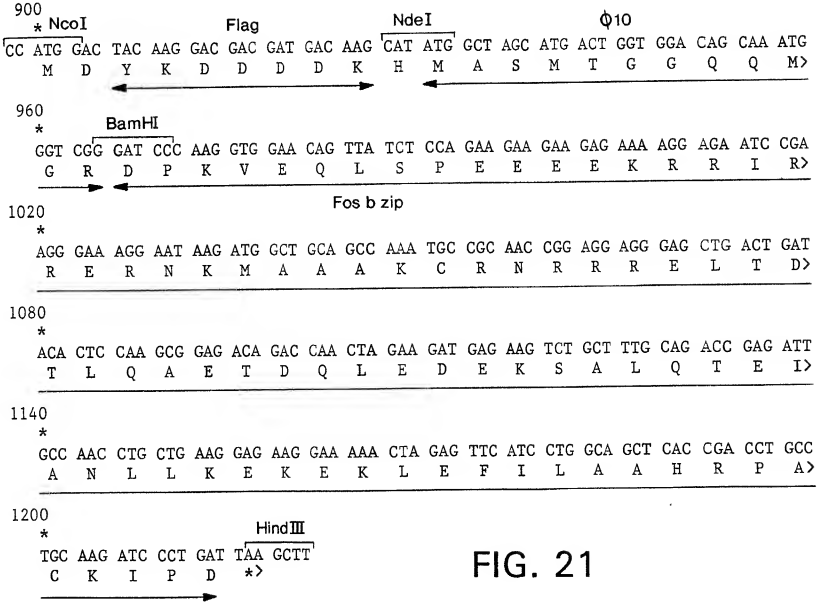
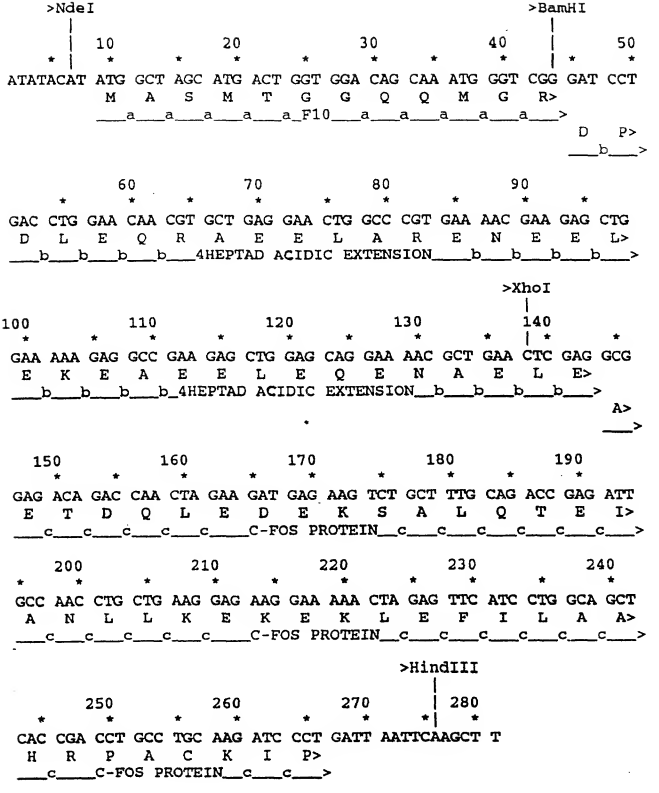

900
* NcoI
Flag
NdeI
ϕ10
CC ATG GAC TAC AAG GAC GAC GAT GAC AAG CAT ATG GCT AGC ATG ACT GGT GGA CAG CAA ATG
M D Y K D D D D K H M A S M T G G Q Q M>
960
*
BamHI
GGT CGG GAT CCC AAG GTG GAA CAG TTA TCT CCA GAA GAA GAA GAG AAA AGG AGA ATC CGA
G R D P K V E Q L S P E E E E K R R I R>
Fos b zip
1020
*
AGG GAA AGG AAT AAG ATG GCT GCA GCC AAA TGC CGC AAC CGG AGG AGG GAG CTG ACT GAT
R E R N K M A A A K C R N R R R E L T D>
1080
*
ACA CTC CAA GCG GAG ACA GAC CAA CTA GAA GAT GAG AAG TCT GCT TTG CAG ACC GAG ATT
T L Q A E T D Q L E D E K S A L Q T E I>
1140
*
GCC AAC CTG CTG AAG GAG AAG GAA AAA CTA GAG TTC ATC CTG GCA GCT CAC CGA CCT GCC
A N L L K E K E K L E F I L A A H R P A>
1200
*
HindIII
TGC AAG ATC CCT GAT TAA GCTT
C K I P D *>

FIG. 21

FIG. 22



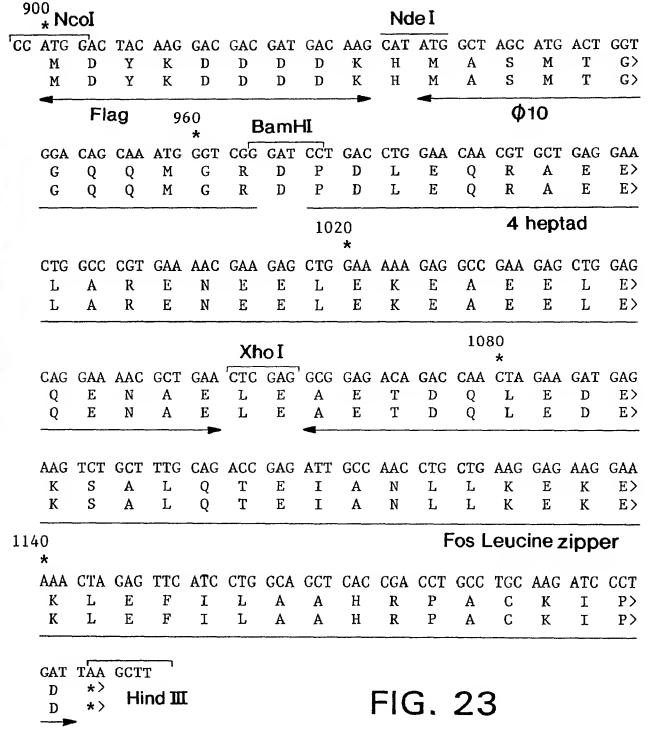

900
NcoI
NdeI
CC ATG GAC TAC AAG GAC GAC GAT GAC AAG CAT ATG GCT AGC ATG ACT GGT
M D Y K D D D D K H M A S M T G>
M D Y K D D D D K H M A S M T G>
Flag
960
BamHI
Φ10
GGA CAG CAA ATG GGT CGG GAT CCT GAC CTG GAA CAA CGT GCT GAG GAA
G Q Q M G R D P D L E Q R A E E>
G Q Q M G R D P D L E Q R A E E>
1020
4 heptad
CTG GCC CGT GAA AAC GAA GAG CTG GAA AAA GAG GCC GAA GAG CTG GAG
L A R E N E E L E K E A E E L E>
L A R E N E E L E K E A E E L E>
XhoI
1080
CAG GAA AAC GCT GAA CTC GAG GCG GAG ACA GAC CAA CTA GAA GAT GAG
Q E N A E L E A E T D Q L E D E>
Q E N A E L E A E T D Q L E D E>
AAG TCT GCT TTG CAG ACC GAG ATT GCC AAC CTG CTG AAG GAG AAG GAA
K S A L Q T E I A N L L K E K E>
K S A L Q T E I A N L L K E K E>
1140
Fos Leucine zipper
AAA CTA GAG TTC ATC CTG GCA GCT CAC CGA CCT GCC TGC AAG ATC CCT
K L E F I L A A H R P A C K I P>
K L E F I L A A H R P A C K I P>
GAT TAA GCTT
D *>
D *>
Hind III

FIG. 23

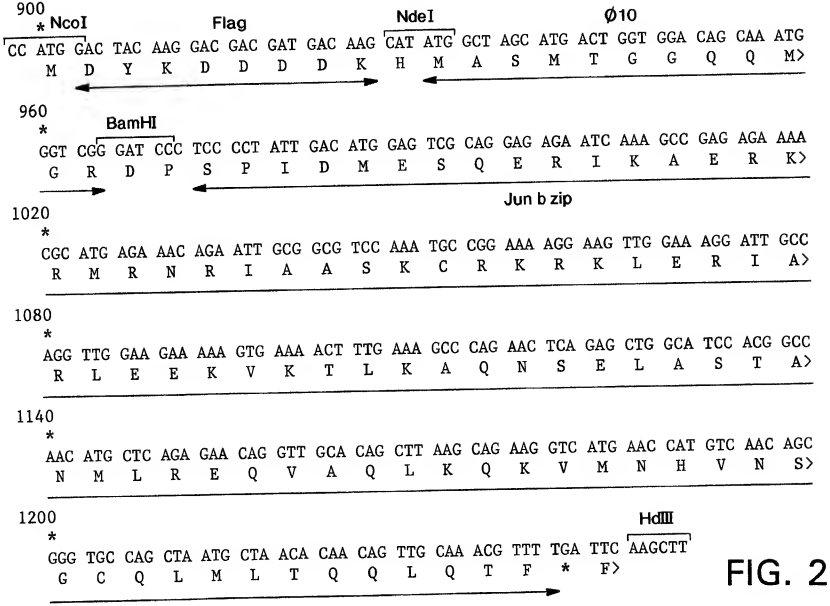


FIG. 24

FIG. 25

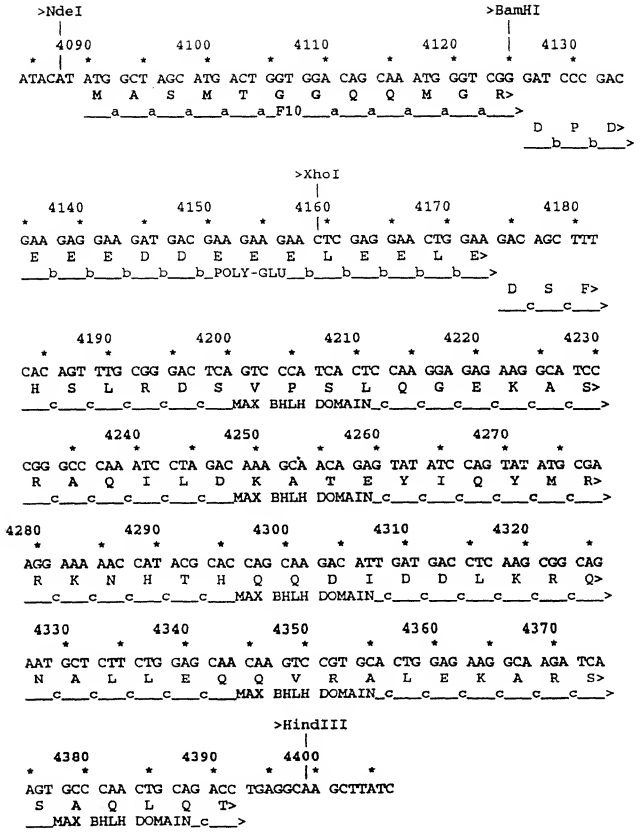


FIG. 26

```
 >NdeI                                                       >BamHI
 |                                                            |
 4090           4100           4110           4120           |   4130
*  |  *          *       *      *       *      *       *      *      *
ATATACAT ATG GCT AGC ATG ACT GGT GGA CAG CAA ATG GGT CGG GAT CCT
          M   A   S   M   T   G   G   Q   Q   M   G   R>
         ____a___a___a___a___a_F10___a___a___a___a___a___>
                                                          D   P>
                                                        ____b___>

                                                                >XhoI
                                                                 |
    4140          4150          4160          4170               |
  *      *      *      *     *      *      *      *      *      |
GAC CTG GAA AAA GAG GCC GAA GAG CTG GAG CAG GAA AAC GCT GAA CTC
 D   L   E   K   E   A   E   E   L   E   Q   E   N   A   E   L>
___b___b__TWO AMPHIPATHIC HEPTAD S (1st PHASE- 783) ___b___b___>

4180          4190          4200          4210          4220
 *      *      *      *      *      *      *      *      *      *
GAG CTG GAA GAC AGC TTT CAC AGT TTG CGG GAC TCA GTC CCA TCA CTC
 E   L   E>
___b___b___>
             D   S   F   H   S   L   R   D   S   V   P   S   L>
            ___c___c___c___c_MAX BHLH DOMAIN___c___c___c___c___>

 4230          4240          4250          4260          4270
  *      *      *      *      *      *      *      *      *      *
CAA GGA GAG AAG GCA TCC CGG GCC CAA ATC CTA GAC AAA GCA ACA GAG
 Q   G   E   K   A   S   R   A   Q   I   L   D   K   A   T   E>
___c___c___c___c___c___MAX BHLH DOMAIN_c___c___c___c___c___c___>

   4280          4290          4300          4310          4320
    *      *      *      *      *      *      *      *      *
TAT ATC CAG TAT ATG CGA AGG AAA AAC CAT ACG CAC CAG CAA GAC ATT
 Y   I   Q   Y   M   R   R   K   N   H   T   H   Q   Q   D   I>
___c___c___c___c___c___MAX BHLH DOMAIN_c___c___c___c___c___c___>

      4330          4340          4350          4360          4370
  *      *      *      *      *      *      *      *      *      *
GAT GAC CTC AAG CGG CAG AAT GCT CTT CTG GAG CAA CAA GTC CGT GCA
 D   D   L   K   R   Q   N   A   L   L   E   Q   Q   V   R   A>
___c___c___c___c___c___MAX BHLH DOMAIN_c___c___c___c___c___c___>

                                                         >HindIII
                                                          |
        4380          4390          4400          4410   |   4420
    *      *      *      *      *      *      *      *   |*      *
CTG GAG AAG GCA AGA TCA AGT GCC CAA CTG CAG ACC TGA GGCAAGCTTA
 L   E   K   A   R   S   S   A   Q   L   Q   T>
___c___c___c___MAX BHLH DOMAIN_c___c___c___c___>

TC
```

FIG. 27

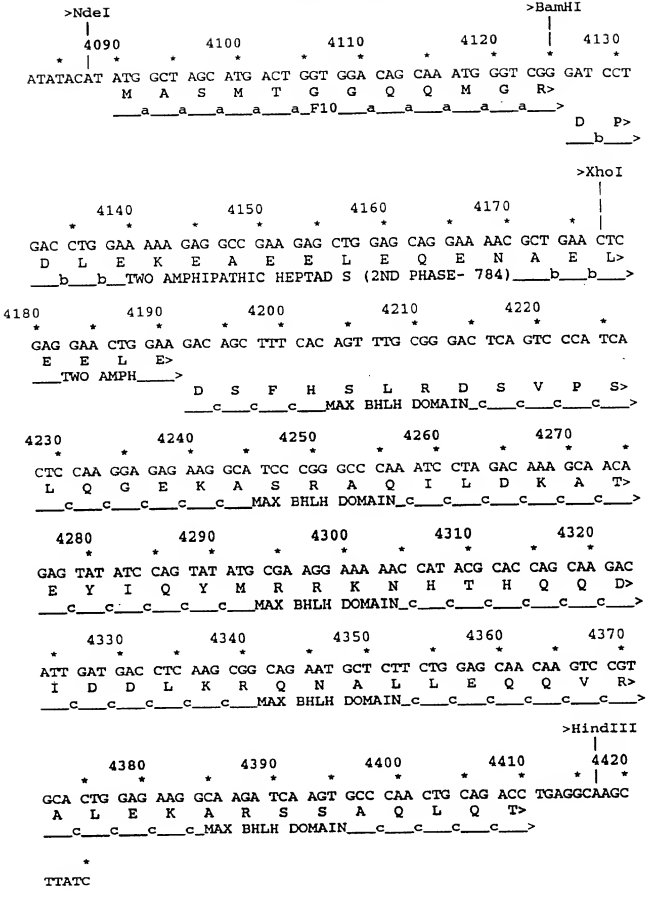
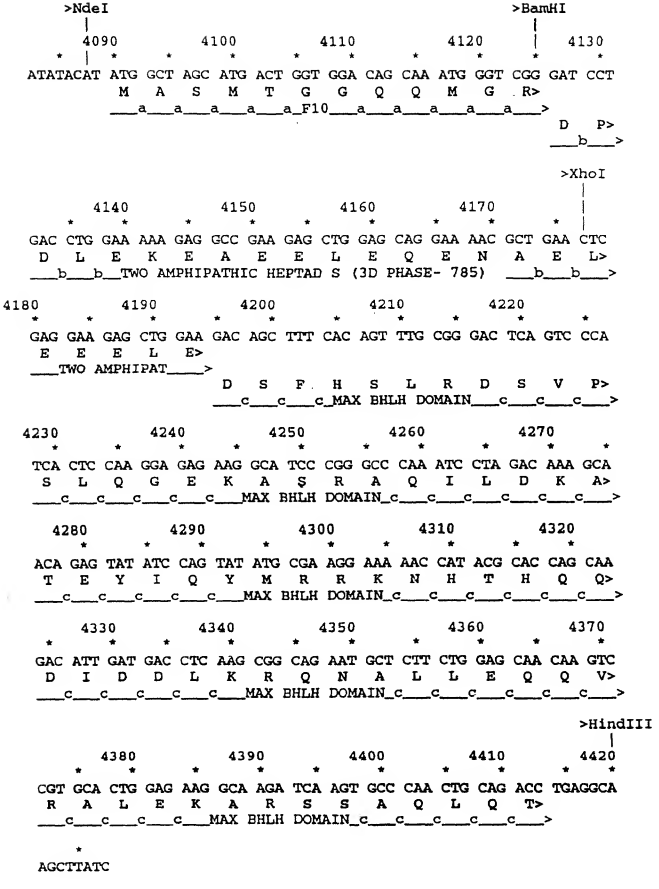


FIG. 28



```
BamHI   10               20               30               40
   *     *       *       *       *       *       *       *       *
GGATCCC AAC GAC AAG AGG CGG ACA CAC AAC GTC TTG GAA CGT CAG AGG
         N   D   K   R   R   T   H   N   V   L   E   R   Q   R>
        ___PUTATIVE;  NCBI GI: 50468; CODON_START=1; C-MYC _____>

50              60               70               80               90
 *       *       *       *       *       *       *       *       *       *
AGG AAC GAG CTG AAG CGC AGC TTT TTT GCC CTG CGT GAC CAG ATC CCT
 R   N   E   L   K   R   S   F   F   A   L   R   D   Q   I   P>
___PUTATIVE;  NCBI GI: 50468; CODON_START=1; C-MYC PROTEIN;_____>

100              110              120              130              140
 *       *       *       *       *       *       *       *       *       *
GAA TTG GAA AAC AAC GAA AAG GCC CCC AAG GTA GTG ATC CTC AAA AAA
 E   L   E   N   N   E   K   A   P   K   V   V   I   L   K   K>
___PUTATIVE;  NCBI GI: 50468; CODON_START=1; C-MYC PROTEIN;_____>

   150              160              170              180              190
    *       *       *       *       *       *       *       *       *
GCC ACC GCC TAC ATC CTG TCC ATT CAA GCA GAC GAG CAC AAG CTC ACC
 A   T   A   Y   I   L   S   I   Q   A   D   E   H   K   L   T>
___PUTATIVE;  NCBI GI: 50468; CODON_START=1; C-MYC PROTEIN;_____>

       200              210              220              230              240
 *       *       *       *       *       *       *       *       *       *
TCT GAA AAG GAC TTA TTG AGG AAA CGA CGA GAA CAG TTG AAA CAC AAA
 S   E   K   D   L   L   R   K   R   R   E   Q   L   K   H   K>
___PUTATIVE;  NCBI GI: 50468; CODON_START=1; C-MYC PROTEIN;_____>

       250              260              270
    *       *       *       *       *       *       *
CTC GAA CAG CTT CGA AAC TCT GGT GCA TAA AAGCTT
 L   E   Q   L   R   N   S   G   A   *>  HindIII
___PUTATIVE;  NCBI GI: 50468; CODON____>
```

FIG. 29

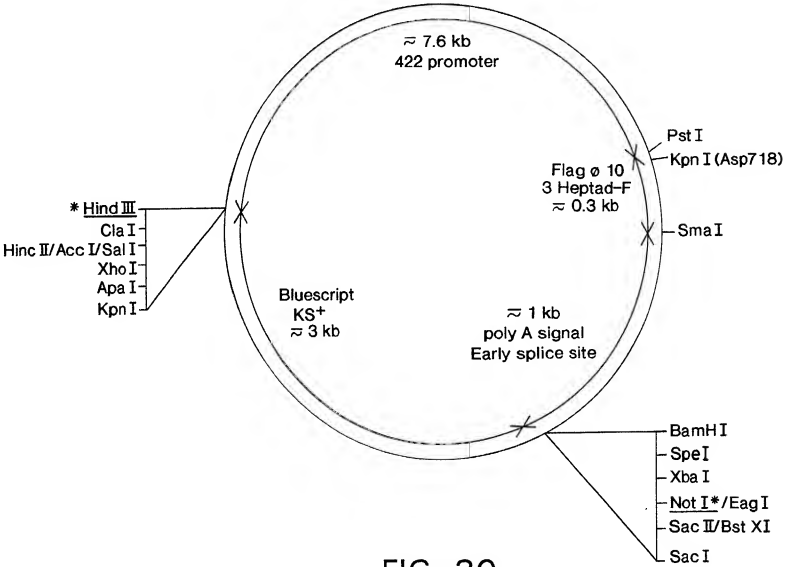


FIG. 30

FIG. 31